

A Mark–Recapture Experiment to Estimate the Escapement of Chinook Salmon in the Blossom River, 2006

by

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Divisions of Sport Fish and Commercial Fisheries



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Weights and measures (metric)		General		Measures (fisheries)	
centimeter	cm	Alaska Department of		fork length	FL
deciliter	dL	Fish and Game	ADF&G	mideye-to-fork	MEF
gram	g	Alaska Administrative		mideye-to-tail-fork	METF
hectare	ha	Code	AAC	standard length	SL
kilogram	kg	all commonly accepted		total length	TL
kilometer	km	abbreviations	e.g., Mr., Mrs., AM, PM, etc.		
liter	L			Mathematics, statistics	
meter	m	all commonly accepted		<i>all standard mathematical</i>	
milliliter	mL	professional titles	e.g., Dr., Ph.D., R.N., etc.	<i>signs, symbols and</i>	
millimeter	mm			<i>abbreviations</i>	
		at	@	alternate hypothesis	H _A
Weights and measures (English)		compass directions:		base of natural logarithm	<i>e</i>
cubic feet per second	ft ³ /s	east	E	catch per unit effort	CPUE
foot	ft	north	N	coefficient of variation	CV
gallon	gal	south	S	common test statistics	(F, t, χ^2 , etc.)
inch	in	west	W	confidence interval	CI
mile	mi	copyright	©	correlation coefficient	
nautical mile	nmi	corporate suffixes:		(multiple)	R
ounce	oz	Company	Co.	correlation coefficient	
pound	lb	Corporation	Corp.	(simple)	r
quart	qt	Incorporated	Inc.	covariance	cov
yard	yd	Limited	Ltd.	degree (angular)	°
		District of Columbia	D.C.	degrees of freedom	df
Time and temperature		et alii (and others)	et al.	expected value	<i>E</i>
day	d	et cetera (and so forth)	etc.	greater than	>
degrees Celsius	°C	exempli gratia		greater than or equal to	≥
degrees Fahrenheit	°F	(for example)	e.g.	harvest per unit effort	HPUE
degrees kelvin	K	Federal Information		less than	<
hour	h	Code	FIC	less than or equal to	≤
minute	min	id est (that is)	i.e.	logarithm (natural)	ln
second	s	latitude or longitude	lat. or long.	logarithm (base 10)	log
		monetary symbols		logarithm (specify base)	log ₂ , etc.
Physics and chemistry		(U.S.)	\$, ¢	minute (angular)	'
all atomic symbols		months (tables and		not significant	NS
alternating current	AC	figures): first three		null hypothesis	H ₀
ampere	A	letters	Jan.,...,Dec	percent	%
calorie	cal	registered trademark	®	probability	P
direct current	DC	trademark	™	probability of a type I error	
hertz	Hz	United States		(rejection of the null	
horsepower	hp	(adjective)	U.S.	hypothesis when true)	α
hydrogen ion activity	pH	United States of		probability of a type II error	
(negative log of)		America (noun)	USA	(acceptance of the null	
parts per million	ppm	U.S.C.	United States	hypothesis when false)	β
parts per thousand	ppt,		Code	second (angular)	"
	‰	U.S. state	use two-letter	standard deviation	SD
volts	V		abbreviations	standard error	SE
watts	W		(e.g., AK, WA)	variance	
				population	Var
				sample	var

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**A MARK-RECAPTURE EXPERIMENT TO ESTIMATE THE
ESCAPEMENT OF CHINOOK SALMON IN THE BLOSSOM RIVER, 2006**

by

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ABSTRACT

The fourth year of a planned 4-year study of Chinook salmon *Oncorhynchus tshawytscha* on the Blossom River was completed in 2006 by the Division of Sport Fish. The study estimated the abundance and age, sex, length composition of large (≥ 660 mm MEF) Chinook salmon in the spawning population. Expansion factors for aerial survey counts of large Chinook salmon were also calculated. Peak counts of large fish can be expanded to account for the proportion of spawners relative to the entire escapement if a specific expansion factor has been estimated for three or more years (PSC 1997), providing a valid technical basis to estimate total escapements from aerial survey counts. Escapement was estimated using a two-event mark-recapture experiment. Fish were captured with rod and reel gear, marked with uniquely numbered spaghetti tags, and batch marked with two secondary marks. Spawning and pre-spawning fish were captured later with angling gear and sampled for marks, age (scales), sex and length. The escapement of large Chinook salmon was estimated to be 1,270 (SE = 172) fish. Age-.3 fish composed an estimated 66% of the escapement estimate of large fish, followed by age-.4 fish (18%), and age-.2 fish (14%). Age-0. fish returning from sub yearling smolt accounted for an estimated 5.9% of the escapement. Females composed an estimated 47.9 % (609) of the escapement of large fish. The calendar year expansion factor for the peak aerial survey count in 2006 was an estimated 3.75 (SE = 0.51), compared to 4.00 (SE = 0.85) in 1998, 2.20 (SE = 0.23) in 2004, and 2.08 (SE = 0.22) in 2005.

Key words: Chinook salmon, *Oncorhynchus tshawytscha*, spawning abundance, escapement, Blossom River, mark-recapture, Petersen model, Markov Chain Monte-Carlo, peak survey count, aerial survey, expansion factor, age, sex, length composition, Behm Canal, Southeast Alaska.

INTRODUCTION

The Blossom River enters the Wilson Arm of Smeaton Bay in the Misty Fjords National Monument about 75 km east of Ketchikan, Alaska (Figure 1). The Blossom River is one of four Behm Canal index streams in the Chinook salmon *Oncorhynchus tshawytscha* escapement estimation program (Pahlke 1998). Prior to 1975, the Blossom River was surveyed on an occasional basis by various methods including foot, boat and fixed-wing aircraft. Since 1975, peak counts (highest count of several single-day counts) of large (≥ 660 mm MEF) Chinook salmon, collected annually by helicopter using a standardized method (time and area), have been used as an index of abundance. Large-sized Chinook salmon are primarily fish age-.3 (saltwater-age-3) or older in most Chinook-producing rivers in Southeast Alaska.

Peak counts of Chinook salmon in the Blossom River have tended to remain near the low end of the revised escapement goal index count range since 1988 (McPherson and Carlile 1997; Figure 2). Temporal trends in the peak counts have been reasonably consistent among the Unuk, Chickamin, Blossom, and Keta rivers, the systems that compose the index sites in Behm Canal

(Pahlke and Magnus. 2006). Relatively low survey counts were observed in 1975–1981 and 1990–2002, and counts were higher between 1982 and 1989. The survey counts in the Blossom River were relatively stable from 1988 to 2005 (mean = 248, SD = 92). All four of the Behm Canal index systems are among the 50 escapement indicator stocks used by the Chinook Technical Committee (CTC) of the Pacific Salmon Commission (PSC) to model population dynamics, and evaluate escapement and management performance.

Beginning in 1998, as part of the State of Alaska's commitment to a coastwide rebuilding and improved stock assessment program for Chinook salmon, the Alaska Department of Fish and Game (ADF&G) Division of Sport Fish obtained funding to estimate the abundance and age, sex and length composition of spawners on the Blossom River. Funding was recommended by the U.S. members of the CTC and approved by the U.S. Commissioners of the PSC, using monies from the U.S. Congress to implement abundance-based management of Chinook salmon from Oregon to Alaska, as detailed in "The 1996 U.S. Letter of Agreement." As determined by two-event mark-recapture (M-R) methodology, the estimated escapement of large Chinook salmon in the Blossom River was 364 (SE = 77) in 1998

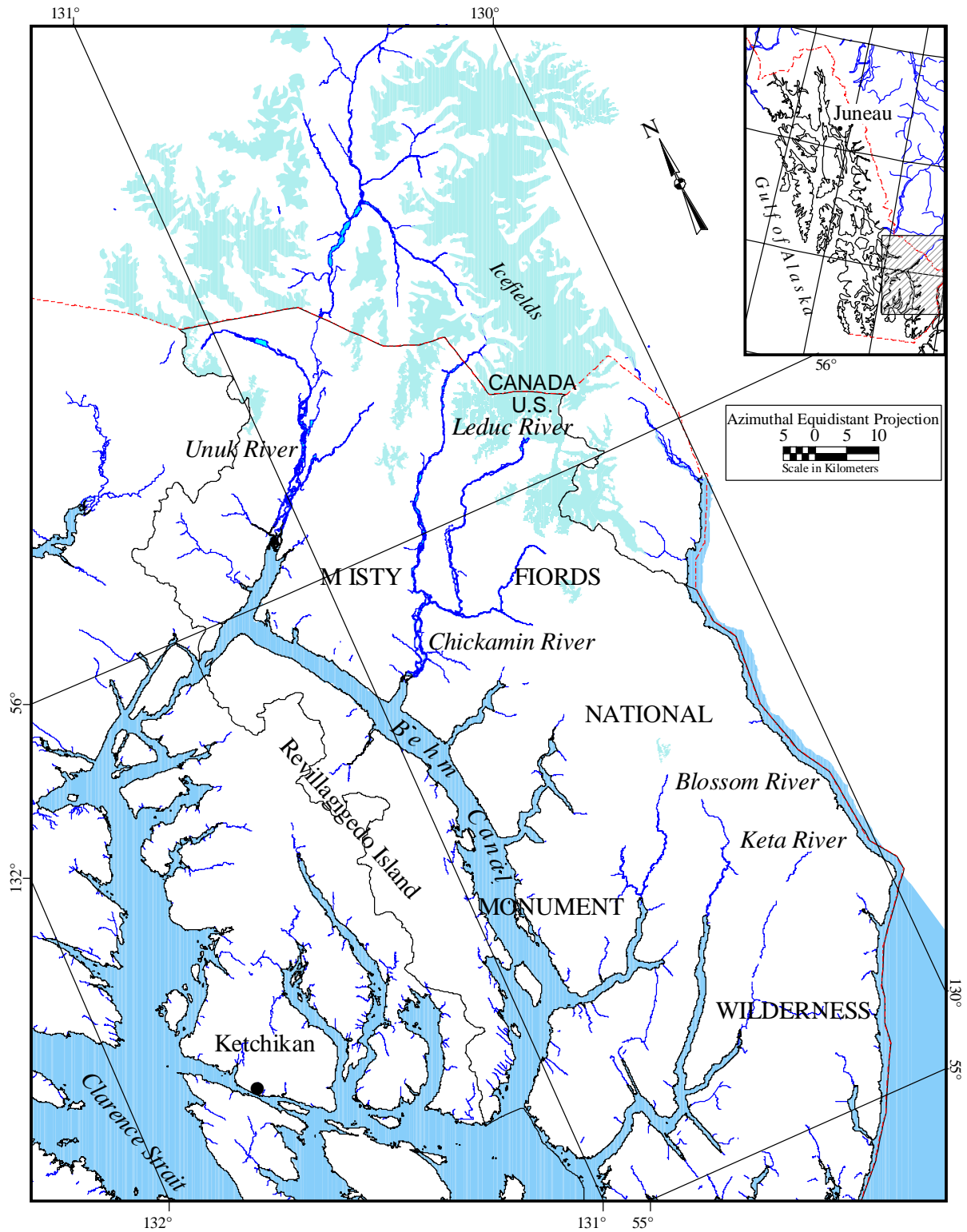


Figure 1.—Behm Canal and Misty Fjords National Monument in Southeast Alaska and location of major Chinook salmon-producing river systems.

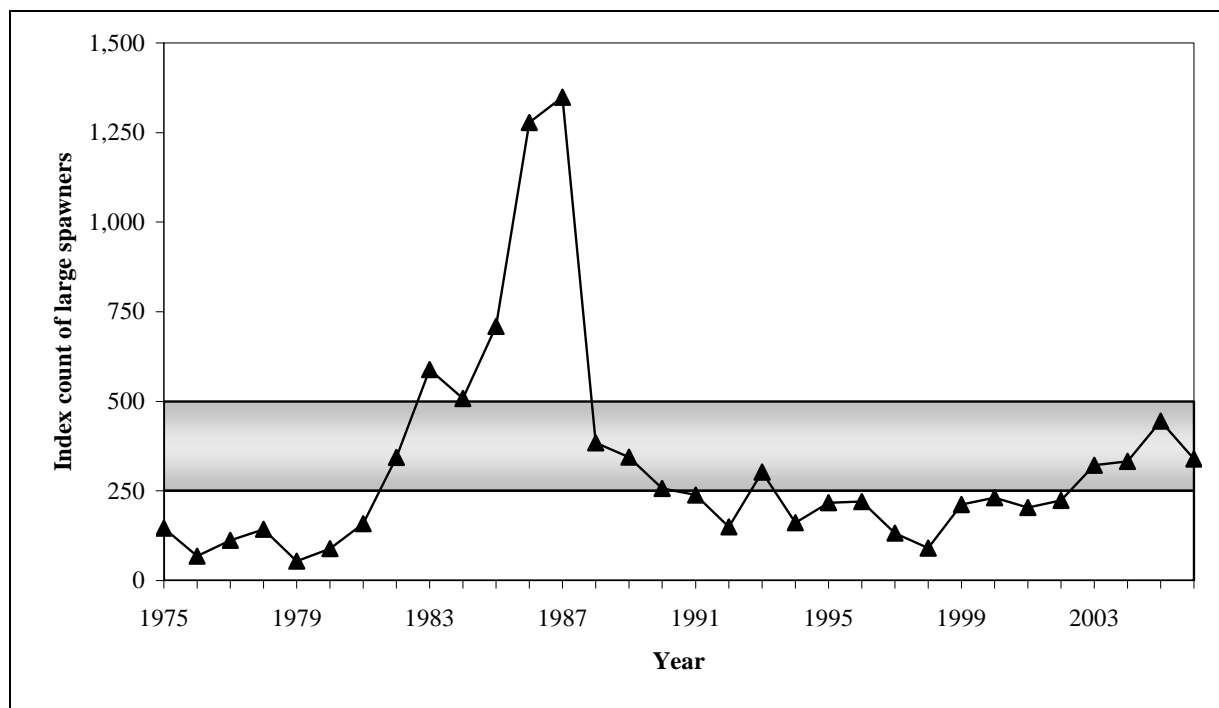


Figure 2.—Peak survey escapement counts (index) of large (≥ 660 mm MEF) Chinook salmon in the Blossom River versus the escapement goal range, 1975–2006. Shaded area is the escapement goal range.

(Brownlee et al. 1999). This was the first Chinook salmon abundance studies conducted on the Blossom River. Budget limitations precluded continuing stock assessment work at the Blossom River until 2004 and 2005. The estimated escapement of large Chinook salmon in the Blossom River was 734 (SE = 76) in 2004 and 926 (SE = 99) in 2005 (Pahlke and Magnus 2005, 2006). The objectives of this project were to estimate abundance and age, sex and length composition of large (≥ 660 mm MEF) Chinook salmon spawning in the Blossom River in 2006.

An estimate of escapement in 2006, along with the annual peak survey count, allowed calculation of an expansion factor for a fourth year, provided data to determine if U.S. CTC escapement data standards (PSC 1997) were met, and provided a valid technical basis to revise estimated total escapements from expanded aerial survey counts. Peak counts of large fish for individual systems can be expanded to account for the proportion of spawners observed in index surveys relative to the entire escapement if a technically valid river specific expansion factor

has been estimated for three or more years (PSC 1997).

STUDY AREA

The Blossom River is tributary to the Wilson Arm of Smeaton Bay, off Behm Canal (Figure 3), draining an area of 176 km². The river is confined within a narrow, steep-sided, glacier-carved valley, and has an overall mainstem gradient of about 1%. The system is defined by short glides, moderate riffles with small cobble and gravel sediments, and long, deep pools. The pool:riffle:glide ratio is about 45:25:30 (Hafele 1983).

There are two large logjams upstream from salt water at about river km (RK) 2 and RK10. Camp was located at RK6, and all gear and personnel were flown in by helicopter during low to normal water levels. Areas above the logjam at river RK10 can be accessed on foot up to about RK15 during low river levels, but a helicopter is needed to get to the upper spawning areas when water levels are above normal. A velocity block at RK17 denies spawners access to the upper 53% of the drainage (Pahlke and Magnus. 2006).

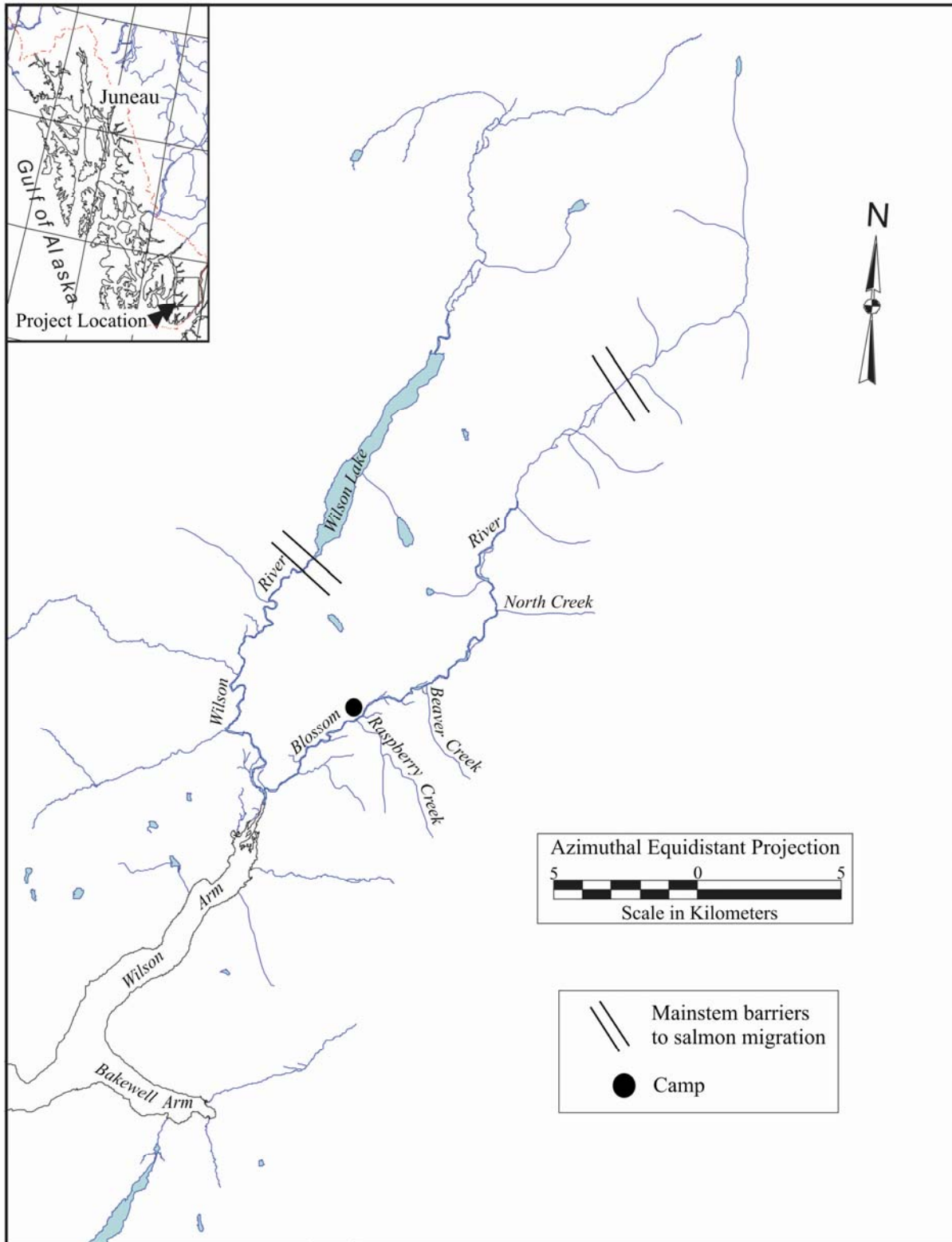


Figure 3.—Blossom River drainage in Southeast Alaska, showing location of major tributaries and barriers to fish migration.

METHODS

A two-event M–R experiment for a closed population (Seber 1982) was conducted on the Blossom River in 2006. Rod and reel angling with bait and lures was the method of capture for the first (capture) event of the experiment in the lower river. Rod and reel snagging and carcass recovery were employed for the second (recapture) event. Previous studies showed this to be an effective means for estimating spawning population parameters in the Blossom River (Brownlee et al. 1999, Pahlke and Magnus 2005, 2006).

MARKING AND SAMPLING

Fish were captured between RK4 and RK8.5 during Event 1. All fish captured in Event 1 were sampled for scales, length to the nearest 5 mm MEF, sex, presence of external parasitic copepods (an indicator of the length of freshwater residence), external color, presence or absence of the adipose fin (indicating the fish was marked with a coded wire tag), and condition. Five scales were taken from each captured fish (Welanders 1940). Scales were mounted onto gum cards; each gum card had the capacity to hold scales from up to 10 fish. The age of each fish was determined later from annual growth patterns of circuli (Olsen 1992) on images of scales impressed onto acetate magnified 70× (Clutter and Whitesel 1956). During the marking phase, a uniquely-numbered solid-core spaghetti tag was applied to each healthy fish ≥ 500 mm MEF length. The tags consisted of a 5.7-cm section of blue, laminated Floy™ tubing shrunk onto a 38-cm piece of 80 lb-test (36.3 kg) monofilament fishing line, modified from a tag design developed and described in Johnson et al. (1992). The tag was applied by first punching the tip portion of a hollow needle through the fish approximately 1.5 cm below and anterior to the insertion of the dorsal fin, so as to be embedded within the last fins rays of the dorsal fin. The tag was pushed into the needle, then the needle withdrawn. A metal leader sleeve was used to secure the ends of the tag line across the fish, below the posterior portion of the dorsal fin. The trailing end of the line was cut 0.5 cm above the crimp. Two secondary (batch) marks consisting of a 0.6-cm punch in the left upper operculum (LUOP) and a left axillary appendage clip (LAA) were applied.

SAMPLING ON THE SPAWNING GROUNDS

Fish were captured from RK3 to approximately RK17 during Event 2. All captured fish were given a left lower operculum punch (LLOP) to prevent double sampling. Fish were examined for the presence of the primary tag, LUOP, LLOP, and LAA, for the absence of their adipose fin, and sampled for length, sex and scales using the same techniques employed during Event 1.

ABUNDANCE ESTIMATE

Conditions which must be met for use of Chapman's modification of the Petersen estimator (Seber 1982) include:

- (a) every fish had an equal probability of being marked in the first sample, or that every fish had an equal probability of being captured in the second sample, or that marked fish mixed completely with unmarked fish; and
- (b) recruitment and mortality did not occur between samples; and
- (c) marking did not affect the catchability of a fish during the second sampling event; and
- (d) fish did not lose their marks in the time between the two samples; and
- (e) all marks were reported on recovery in the second sample; and
- (f) double sampling did not occur.

Condition (a) may be violated if size- or sex-selective sampling occurs. Kolmogorov-Smirnov (K-S) two-sample tests were used to test the hypothesis that fish of different lengths were captured with equal probability during both first and second sampling events. These test procedures are described in Appendix A1, as well as corrective measures (stratification) based on diagnostic test results that minimize bias in estimation of abundance and composition parameters. Gender bias was tested using two chi-square tests. In the first test, selectivity during the second sampling event is determined by comparing the number of fish of each gender marked in Event 1 and recaptured in Event 2 to the number marked and not recaptured. In the second test, the numbers of fish of each gender marked in Event 1 and inspected for marks in Event 2 are compared to determine if selectivity

occurred in the first sampling event. Use of these tests assumes gender is accurately determined in each event. To test this assumption, the gender of each recaptured fish is compared to gender assigned in Event 1. If gender is assigned the same in Event 1 and Event 2, we presume there was no error in assigning gender during Event 1.

Three consistency tests (Appendix A2) described by Seber (1982) were used to test for temporal and/or spatial violations of condition (a). Contingency table analyses were used to test three null hypotheses: 1) the probability that a marked fish is recovered during Event 2 is independent of when it was marked; 2) the probability that a fish inspected during Event 2 is marked is independent of when/where it was caught during the second event; and 3) for all marked fish recovered during Event 2, time of marking is independent of when/where recovery occurs. If all three hypotheses are rejected, the “partially” stratified abundance estimator described by Darroch (1961) must be used. Failure to reject at least one of these three hypotheses was sufficient to conclude that at least one of the conditions in (a) was satisfied, and a Petersen-type model was appropriate to estimate abundance.

The experiment was assumed closed to recruitment because sampling spanned the entire immigration. Marking was assumed to have little effect on behavior of released fish or the catchability of fish on the spawning grounds because only healthy fish were tagged and released, and because radio telemetry studies conducted concurrent with Chinook salmon M–R studies on six rivers in the region have shown that little (a maximum of 5–9%) tag-induced mortality occurs in the marking event for Chinook salmon (Pahlke et al. 1996). The use of multiple marks during Event 1, careful inspection of all fish captured during Event 2, and additional marking of all fish inspected helped to insure that conditions (d), (e), and (f) were met.

Abundance of large Chinook salmon on the spawning grounds was estimated with the Chapman (1951) modified Petersen estimator (Seber 1982). Estimated abundance was calculated as:

$$\hat{N} = \frac{(n_1 + 1)(n_2 + 1)}{(m_2 + 1)} - 1 \quad (1)$$

where:

- \hat{N} = estimated abundance of large (≥ 660 mm MEF) Chinook salmon in the Blossom River;
- n_1 = the number of large Chinook salmon tagged and released during the first sampling event;
- n_2 = the number of large Chinook salmon inspected for marks during the second sampling event; and,
- m_2 = the number of marked large Chinook salmon detected during second event sampling.

Variance for the estimator (equation 1) was estimated using empirical Bayesian methods (Carlin and Louis 2000). Using Markov Chain Monte-Carlo (MCMC) techniques, a posterior distribution for \hat{N} was generated by collecting 100,000 simulated values of $\hat{N}_{(b)}$ which were calculated using equation (1) from simulated values of equation parameters. Simulated values were modeled from observed data using a multinomial distribution of \hat{N} experimental fish with the multinomial components: $(n_1 - n_2)$, $(n_2 - m_2)$, (m_2) , and $(\hat{N} - n_1 - n_2 + m_2)$. At the end of the iterations, the following statistics were generated:

$$\bar{N} = \frac{\sum_{b=1}^{100,000} \hat{N}_{(b)}}{100,000} \quad (2)$$

and,

$$\hat{var}(\hat{N}) = \frac{\sum_{b=1}^{100,000} (\hat{N}_{(b)} - \bar{N})^2}{100,000 - 1} \quad (3)$$

EXPANSION FACTOR

Standardized, low altitude helicopter surveys have been used to count large Chinook salmon in the Blossom River since 1975 (Pahlke 1998). During years when both M–R estimates and aerial counts

were available (1998 and 2004–2006), an abundance-to-count annual expansion factor ($\hat{\pi}_i$) for large Blossom River Chinook salmon was estimated:

$$\hat{\pi}_i = \hat{N}_i / C_i \quad (4)$$

$$\hat{v}ar(\hat{\pi}_i) = \hat{v}ar(\hat{N}_i) / C_i^2 \quad (5)$$

where \hat{N}_i is the M–R estimate of large Chinook salmon in year i and C_i is the peak aerial survey count in year i .

For return years when M–R estimates were not available, a long-term expansion factor is used to estimate total escapement of large Chinook salmon. The long-term observed expansion factor ($\bar{\pi}$) is estimated as:

$$\bar{\pi} = \frac{\sum_{y=1}^k \hat{\pi}_y}{k} \quad (6)$$

$$\begin{aligned} \hat{v}ar(\bar{\pi}) &= \hat{v}ar_B(\hat{\pi}) - \frac{\sum_{y=1}^k \hat{v}ar(\hat{\pi}_y)}{k} \\ &+ \hat{v}ar_B(\bar{\pi}) \end{aligned} \quad (7)$$

where k is the number of years with both counts and M–R estimates and $\hat{\pi}_y$ is the observed expansion factor in year y . The estimate of $\hat{v}ar(\bar{\pi})$ is the appropriate term for predicting a new value of π , and the measurement error within years (i.e., the M–R induced error in escapement estimation) has been removed (see Appendix A3 for details).

The estimator for expanding peak survey counts into estimates of spawning abundance in year t without a M–R estimate is:

$$\hat{N}_t = \bar{\pi}_t C_t \quad (8)$$

$$\hat{v}ar(\hat{N}_t) = C_t^2 \hat{v}ar(\bar{\pi}) \quad (9)$$

where C_t is the peak aerial survey count in year t .

AGE AND SEX COMPOSITION

The proportion of the spawning population of large Chinook salmon composed of a given age j was estimated as a binomial variable:

$$\hat{p}_j = \frac{n_j}{n} \quad (10)$$

$$\hat{v}ar(\hat{p}_j) = \frac{\hat{p}_j(1 - \hat{p}_j)}{n - 1} \quad (11)$$

where \hat{p}_j is the estimated proportion of age j fish in the population, n is the sample size, and n_j is the number of fish of age j in the sample (note: $\sum_j \hat{p}_j = 1$). Information from both events was pooled to estimate age and gender composition of large Chinook salmon, as no size selectivity in either event was detected, and gender was accurately determined. Numbers of spawning fish by age were estimated as the sum of the products of estimated age composition and estimated abundance:

$$\hat{N}_j = \hat{p}_j \hat{N} \quad (12)$$

$$\begin{aligned} \hat{v}ar(\hat{N}_j) &= \hat{v}ar(\hat{p}_j) \hat{N}^2 + \\ &\hat{v}ar(\hat{N}) \hat{p}_j^2 - \hat{v}ar(\hat{p}_j) \hat{v}ar(\hat{N}) \end{aligned} \quad (13)$$

where the variance is for a product of two independent variables (Goodman 1960).

Age and sex composition for the entire spawning population and its associated variances were also estimated by first redefining the binomial variables in samples to produce estimated proportions by sex \hat{p}_q , where q denotes gender (male or female), such that $\sum_q \hat{p}_q = 1$, and by age-sex \hat{p}_{jq} , such that $\sum_{jq} \hat{p}_{jq} = 1$.

RESULTS

TAGGING, RECOVERY AND ABUNDANCE

Between 7 July and 2 August, 250 Chinook salmon were captured, sampled, and released with spaghetti tags and batch marks in the Blossom River. An additional 10 fish (5 medium, 4 large, and 1 fish of undetermined length) were captured and sampled for age (scales), sex, and length (ASL) data, but either escaped prior to marking or were determined to be in “poor” health and were consequently not marked. Of the 250 marked fish, 29 were medium sized (500–659 mm MEF), 220 were large (≥ 660 mm MEF), and one fish was not measured for length (Table 1). In addition, 59 small (<500 mm MEF) fish were captured and sampled for ASL data, but not tagged.

From 16 August through 27 August, 2 small, 6 medium, 229 large, and 1 fish of unknown length were captured and inspected for marks during Event 2 (Table 1). Of these, 1 medium and 39 large fish were observed with marks (Table 1). Fish less than 660 mm MEF were not used in abundance or age calculations because only 1 fish <660 mm MEF was recaptured in Event 2. Two of the numbers on spaghetti tags from large recaptured fish were mis-recorded.

The cumulative relative frequencies (crfs) for lengths of large fish marked in Event 1 and those recaptured on the spawning grounds were not significantly different (K-S test, D-value = 0.092, $P = 0.914$; Figure 4). Similarly, no difference was detected between fish inspected for marks on the spawning grounds and those marked fish recaptured on the spawning grounds (D-value = 0.113, $P = 0.728$; Figure 4). These results suggest little evidence of size bias sampling for large fish during either sampling event. Therefore, length stratification of the experiment

was not needed to estimate abundance of large fish (Appendix A1). We also determined that sex selectivity did not occur during either sampling event, on the basis of gender frequencies of fish recovered and not recovered in Event 2 ($\chi^2 = 0.183$, $P = 0.670$, $df = 1$), and fish marked in Event 1 and examined in Event 2 ($\chi^2 = 0.001$, $P = 0.975$, $df = 1$). However, the gender assigned to 1 of 39 (2.6%) large recaptured fish differed from what had been assigned in Event 1. Consequently, only large fish sampled during Event 2 were used for estimating abundance by sex and age (Appendix A1).

A chi-square test of the hypothesis that marked and unmarked fractions of large fish were independent of spatial recovery strata yielded a non-significant result ($\chi^2 = 1.028$, $df = 2$, $P = 0.598$; Table 2). Another chi-square test of the hypothesis that the probability of recapture of large marked fish was independent of the marking strata was also non-significant ($\chi^2 = 0.040$, $df = 2$, $P = 0.980$; Table 2). Failure to reject the null hypothesis for either of these two tests was sufficient to allow use of a Petersen-type estimator (Arnason et al. 1996).

The abundance of large fish was estimated as $\hat{N} = 1,270$ fish (SE = 172; Table 3) based on $n_1 = 220$ large fish marked in the first event, $n_2 = 229$ inspected in the second event, and $m_2 = 39$ recaptured (Table 2). The 95% confidence interval for the estimated abundance of large fish is 933–1,607 (Table 3).

ESTIMATES OF AGE, SEX AND LENGTH COMPOSITION

No evidence of size-selective sampling was detected for large Chinook salmon in either event (see diagnostic results above). However, one large marked fish recaptured during Event 2 had been

Table 1.—Numbers of Chinook salmon captured and marked or not marked during Event 1, and inspected for marks and recaptured during Event 2, on the Blossom River in 2006, by size class.

		Medium		Large	Not measured	Total
		<500 mm MEF	500–659 mm MEF	≥ 660 mm MEF		
Event 1	Captured	59	34	224	2	319
	Marked		29	220	1	250
	Not marked	59	5	4	1	69
Event 2	Inspected	2	6	229	1	238
	Marked		1	39		40

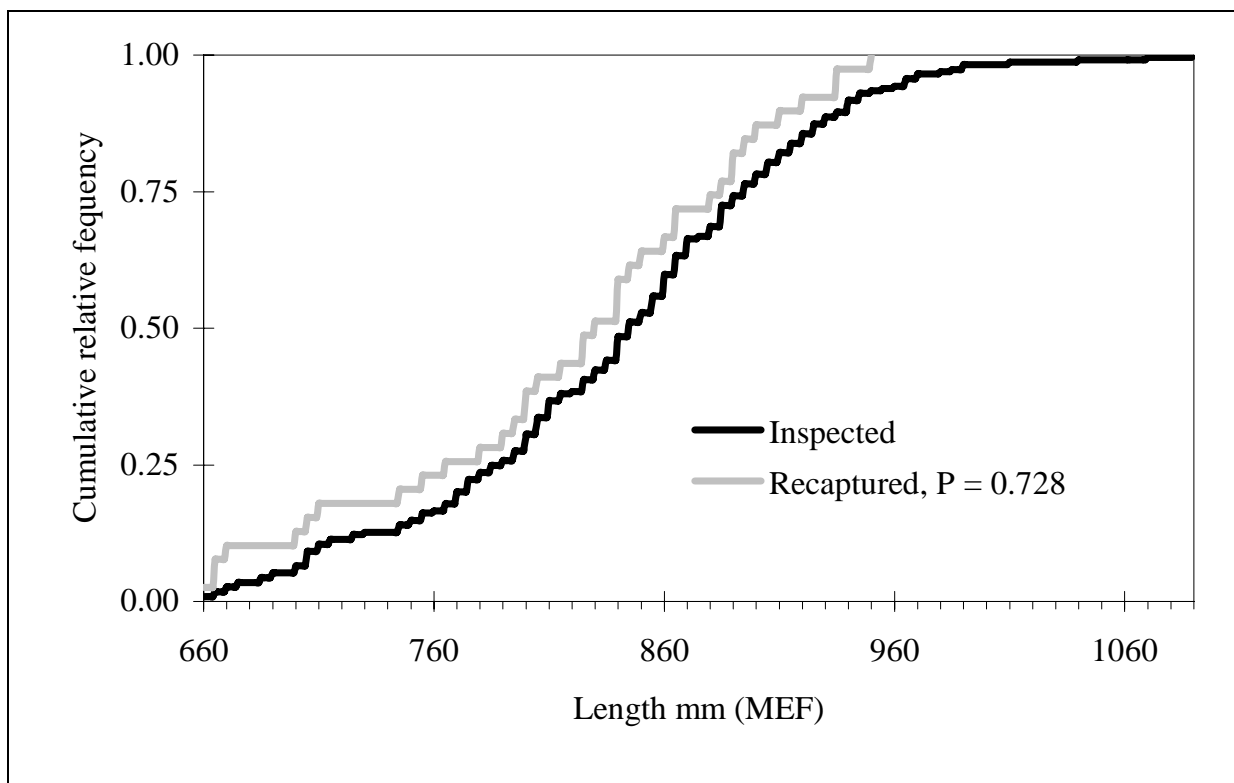
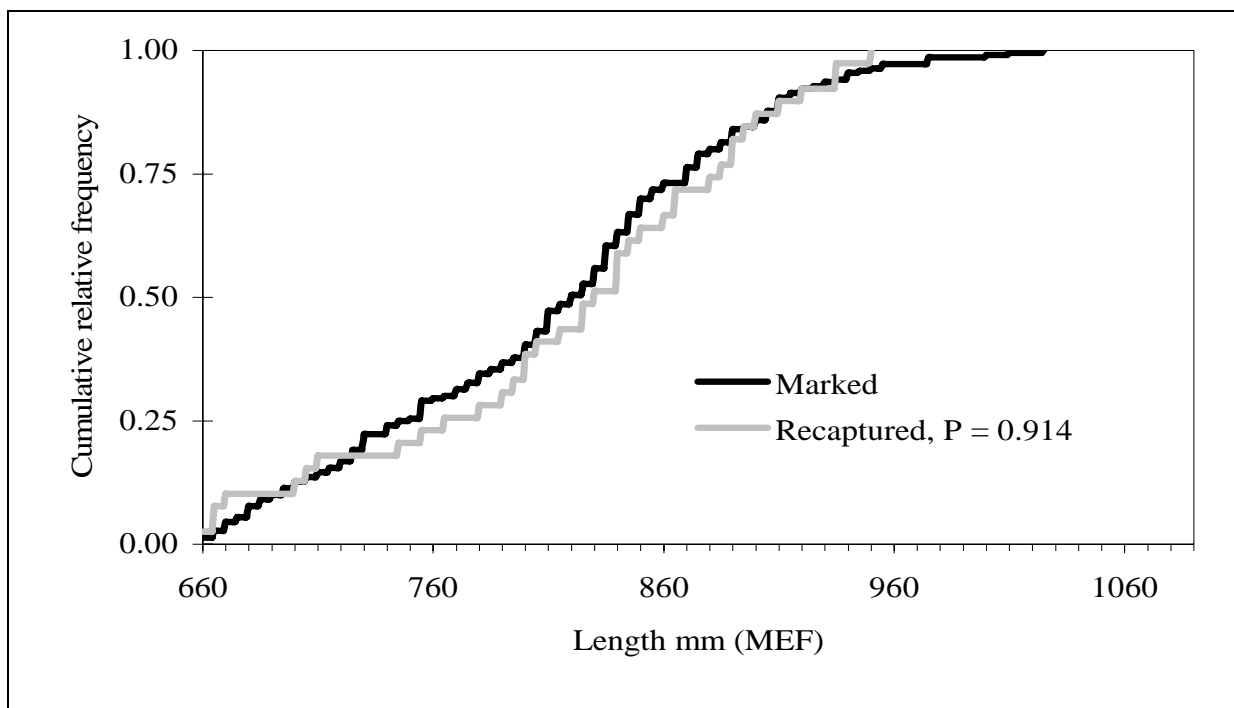


Figure 4.—Cumulative relative frequencies of large (≥ 600 mm MEF) Chinook salmon marked during Event 1 and recaptured during Event 2 (upper graph), and inspected and recaptured during Event 2 (lower graph) in the Blossom River, 2006.

Table 2.—Numbers of marked large (≥ 660 mm MEF; PANEL A) and medium (500–659 mm MEF; PANEL B) Chinook salmon released in the Blossom River in 2006, by marking period, and the number inspected for marks and recaptured by recovery location.

PANEL A: LARGE (>659 mm MEF) CHINOOK SALMON						
Marking date	Number marked	Recovery location			Total	Fraction recovered
		RK <10	RK 10-14	RK >14		
July 7–July 17	75	5	8		13	0.173
July 18–July 26	68	3	2	4	9	0.132
July 27–August 2	77	8	6	1	15	0.195
Total	220	17 ^a	16	6 ^a	39	0.177
Number inspected		100	96	33	229	
Fraction marked		0.170	0.167	0.182	0.170	

PANEL B: MEDIUM (500–659 mm MEF) CHINOOK SALMON						
Marking date	Number marked	Recovery location			Total	Fraction recovered
		RK <10	RK 10-14	RK >14		
July 7–July 17	9	1			1	0.111
July 18–July 26	6					0.000
July 27–August 2	14					0.000
Total	29	1			1	0.034
Number inspected		4	1	1	6	
Fraction marked		0.250			0.167	

^a Includes one recovery of unknown marking date.

Table 3.—Peak survey counts, mark–recapture estimates of escapement, and estimated expansion factors for large (≥ 660 mm MEF) Chinook salmon in the Blossom River in 1998 and 2004–2006.

Parameter	Year				Average (all years)	Average (1998 and 2006)	Average (2004 and 2005)
	1998	2004	2005	2006			
Survey conditions	Normal	Excellent	Excellent	Normal	All	Normal	Excellent
Survey count	91	333	445	339	302	215	389
Mark-recapture estimate (M–R)	364	734	926	1,270	824	817	830
M–R standard error	77	76	99	172	106	125	88
95% RP M–R estimate	41.5	20.3	21.0	26.5	27.3	34.0	20.6
M–R lower 95% C.I.	292	609	791	933	656	573	659
M–R upper 95% C.I.	597	908	1,148	1,607	1,065	1,061	1,002
Survey count/M–R estimate (%)	25.0	45.4	48.1	26.7	36.3	25.8	46.7
Expansion factor (EF)	4.00	2.20	2.08	3.75	3.01	3.87	2.14
SE (EF)	0.85	0.23	0.22	0.51	1.03	0.62	0.19
CV (EF)	21.2	10.4	10.7	13.5	34.3	16.1	9.0

assigned the opposite sex in Event 1. This infers error in sex assignment of fish in Event 1, and a lack of confidence in comparing sex compositions in Event 1 and Event 2. As a result, only samples from Event 2 were used for estimating age and sex composition, and mean length at age and sex (*Case III*, Appendix A1). Estimates of age and sex composition and mean length at age were only calculated for large Chinook salmon. When

discrepancies occurred in lengths of recaptured fish between Events 1 and 2, Event 1 lengths were used for diagnostic tests and estimates of abundance and composition.

Age-1.3 Chinook salmon from the 2001 brood year dominated the escapement of large fish (60.9%, SE = 3.8%) in the Blossom River in 2006 (Table 4). Age-1.4 (17.8%, SE = 2.9%) and age-1.2 fish (14.2%, SE = 2.7%) accounted for the

Table 4.—Estimated age and sex composition and escapement of large (≥ 660 mm MEF) Chinook salmon in the Blossom River, 2006. Estimates are from Chinook salmon sampled on the spawning grounds during Event 2.

		Brood year and age class						Total
		2002 1.2	2002 0.3	2001 1.3	2001 0.4	2000 1.4	1999 1.5	
Males	Sample size	24	6	49		8	1	88
	$p_{ijk} \times 100$	14.2	3.6	29.0		4.7	0.6	52.1
	$SE(p_{ijk}) \times 100$	2.7	1.4	3.5		1.6	0.6	3.9
	N_{ijk}	180	45	368		60	8	661
	$SE(N_{ijk})$	42	19	67		22	8	102
Females	Sample size		3	54	1	22	1	81
	$p_{ijk} \times 100$		1.8	32.0	0.6	13.0	0.6	47.9
	$SE(p_{ijk}) \times 100$		1.0	3.6	0.6	2.6	0.6	3.9
	N_{ijk}		23	406	8	165	8	609
	$SE(N_{ijk})$		13	71	8	40	8	96
Total	Sample size	24	9	103	1	30	2	169
	$p_{ij} \times 100$	14.2	5.3	60.9	0.6	17.8	1.2	100.0
	$SE(p_{ij}) \times 100$	2.7	1.7	3.8	0.6	2.9	0.8	
	N_{ij}	180	68	774	8	225	15	1,270
	$SE(N_{ij})$	42	24	115	8	48	11	172

bulk of the remainder. Males composed 52.1% (SE = 3.9%) of the escapement of fish ≥ 660 mm MEF, and all age-1.2 fish sampled were males. There were an estimated 609 (SE = 96) females in the spawning population of large fish, and age-1.3 fish were the most abundant age class amongst females. Of the 169 scale samples from Event 2 that were successfully aged, 159 (94%) were age-1. fish from yearling smolt; the remaining 10 fish were age-0 (Table 4).

Average length-at-age generally increased with saltwater age for both male and female Chinook salmon sampled (Table 5, Figure 5). Within age-1.3 fish, females were on average 30 mm longer than males, whereas age-1.4 males averaged an estimated 92 mm longer than their female counterparts. Summary statistics for ages of all fish sampled during each event are shown in Appendix A4.

EXPANSION FACTOR

The expansion factor for the Blossom River Chinook salmon aerial surveys was calculated as the annual ratio of the estimate of abundance of large Chinook salmon to the peak aerial survey count for the individual year. The estimated expansion factor in 2006 was 3.75 (SE = 0.51), compared to 4.0 (SE = 0.85) in 1998, 2.20 (SE = 0.23) in 2004 and 2.08 (SE = 0.22) in 2005 (Table

3). The estimated mean expansion factor was 3.01 (SE = 1.03).

Survey conditions were rated excellent for the Blossom River in 2004 and 2005 and normal during 1998 and 2006 (Pahlke 2007). The average expansion factor for the two years with normal survey conditions was 3.87 (SE = 0.62), and for the two years with excellent survey conditions it was 2.14 (SE = 0.19) (Table 3). The sensitivity of counting efficiency to survey conditions renders the mean expansion factor a less accurate predictor than the condition-based expansion factors; for years without annual count to M–R estimates and with recorded survey conditions, use of the later is preferred. Estimates of spawning abundance in the Blossom River ranged from 163 in 1979 to 4,060 in 1987 (Table 6, Figure 6).

DISCUSSION

The data standards developed by the U.S. section of the CTC (PSC 1997) require that expansion factors be estimated a minimum of three times. Annual expansion factors for counts of large Chinook salmon in the Blossom River have now been estimated four times, resulting in an estimated mean EF = 3.01. However the mean expansion factor is not as accurate as those estimated for other nearby systems such as the

Table 5.—Estimated average length (mm MEF) by sex and age of the escapement of large (≥ 660 mm MEF) Chinook salmon in the Blossom River, 2006. Estimates are from Chinook salmon sampled on the spawning grounds during Event 2.

		Brood year and age class						Total
		2002 0.3	2002 1.2	2001 0.4	2001 1.3	2000 1.4	1999 1.5	
Males	Sample size	6	24		49	8	1	88
	Avg. length	829	701		822	987	965	806
	SD	73	30		79	79		105
	SE	30	6		11	28		11
Females	Sample size	3		1	54	22	1	81
	Avg. length	858		870	852	895	970	865
	SD	55			40	40		45
	SE	32			5	8		5
Total	Sample size	9	24	1	103	30	2	169
	Avg. length	839	701	870	837	919	968	834
	SD	66	30		63	66	4	87
	SE	22	6		6	12	3	7

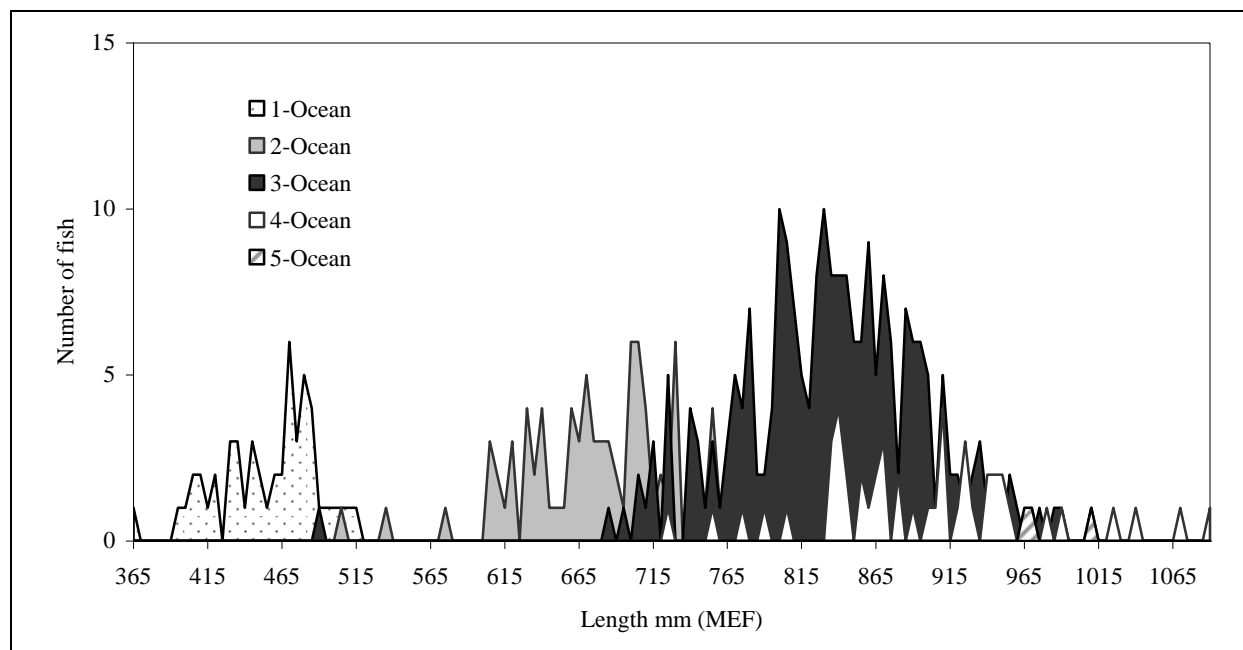


Figure 5.—Number of Chinook salmon by ocean age and length (mm MEF) from the Blossom River 2006. Includes all fish from both events from which age and length were determined, with the exception of one 230 mm MEF age-2.0 fish sampled during Event 1.

Unuk and Chickamin rivers due to the greater sensitivity of index counts on the Blossom River to survey conditions. As a result, annual expansion factors for the Blossom River exhibit a bimodal characteristic; expansion factors for years with normal survey conditions are roughly double those in years with excellent survey conditions.

Index counts on the Unuk and Chickamin rivers are the summed counts from multiple spawning tributaries in contrast to the Blossom River where counts are conducted on a single 15 kilometer stretch of main stem river. The same river and atmospheric conditions that create favorable survey conditions in some tributaries of the Unuk

Table 6.—Peak survey counts, survey conditions, preferred expansion factors, and estimates of spawning abundance of large (≥ 660 mm MEF) Chinook salmon in the Blossom River, 1975–2006.

Year	Peak Count From Surveys	Survey Conditions ^a	Preferred Expansion Factor (EF) ^b	SE (EF)	Abundance Estimated from Expanded Count		Abundance Estimated from M–R Experiment		Preferred Abundance Estimate	
					N	SE (N)	N	SE (N)	N	SE (N)
1975	146		3.01	1.03	439	150			439	150
1976	68		3.01	1.03	205	70			205	70
1977	112		3.01	1.03	337	115			337	115
1978	143		3.01	1.03	430	147			430	147
1979	54		3.01	1.03	163	56			163	56
1980	89		3.01	1.03	268	92			268	92
1981	159		3.01	1.03	479	164			479	164
1982	343		3.01	1.03	1,032	353			1,032	353
1983	589		3.01	1.03	1,773	607			1,773	607
1984	508		3.01	1.03	1,529	523			1,529	523
1985	709		3.01	1.03	2,134	730			2,134	730
1986	1,278		3.01	1.03	3,847	1,316			3,847	1,316
1987	1,349		3.01	1.03	4,060	1,389			4,060	1,389
1988	384		3.01	1.03	1,156	396			1,156	396
1989	344		3.01	1.03	1,035	354			1,035	354
1990	257		3.01	1.03	774	265			774	265
1991	239	normal	3.87	0.62	925	148			925	148
1992	150	normal	3.87	0.62	581	93			581	93
1993	303	normal	3.87	0.62	1,173	188			1,173	188
1994	161	normal	3.87	0.62	623	100			623	100
1995	217	normal	3.87	0.62	840	135			840	135
1996	220	excellent	2.14	0.19	471	42			471	42
1997	132	normal	3.87	0.62	511	82			511	82
1998	91	normal	4.00	0.85	364	77	364	77	364	77
1999	212	normal	3.87	0.62	820	131			820	131
2000	231	normal	3.87	0.62	894	143			894	143
2001	204	normal	3.87	0.62	789	126			789	126
2002	224	excellent	2.14	0.19	479	43			479	43
2003	322	excellent	2.14	0.19	689	61			689	61
2004	333	excellent	2.20	0.23	734	76	734	76	734	76
2005	445	excellent	2.08	0.22	926	99	926	99	926	99
2006	339	normal	3.75	0.51	1,270	172	1,270	172	1,270	172

^a Pahlke 2007.

^b Preferred EF is the estimated annual EF for years with counts and M–R estimates of abundance (1998, 2004–2006), the mean EF (3.01) for years with neither M–R estimates nor recorded survey conditions, and the average estimated EF, by survey condition, for years without M–R estimates of abundance but with known survey conditions rated normal (EF = 3.87) or excellent (EF = 2.14)

or Chickamin rivers can result in less than favorable conditions in other tributaries within the same watershed, and vice versa, creating an overall buffering effect on the index counts from these systems. Survey conditions on the Blossom River however will be fundamentally uniform throughout the survey area, and consequently survey counts will be more sensitive to survey

conditions than on “buffered” systems such as the Unuk or Chickamin rivers.

The methodology used in this M–R study to estimate the abundance of large Chinook salmon has been proven effective. However, it has not been very effective at estimating the abundance of the spawning population less than 660 mm MEF in length, predominantly due to our

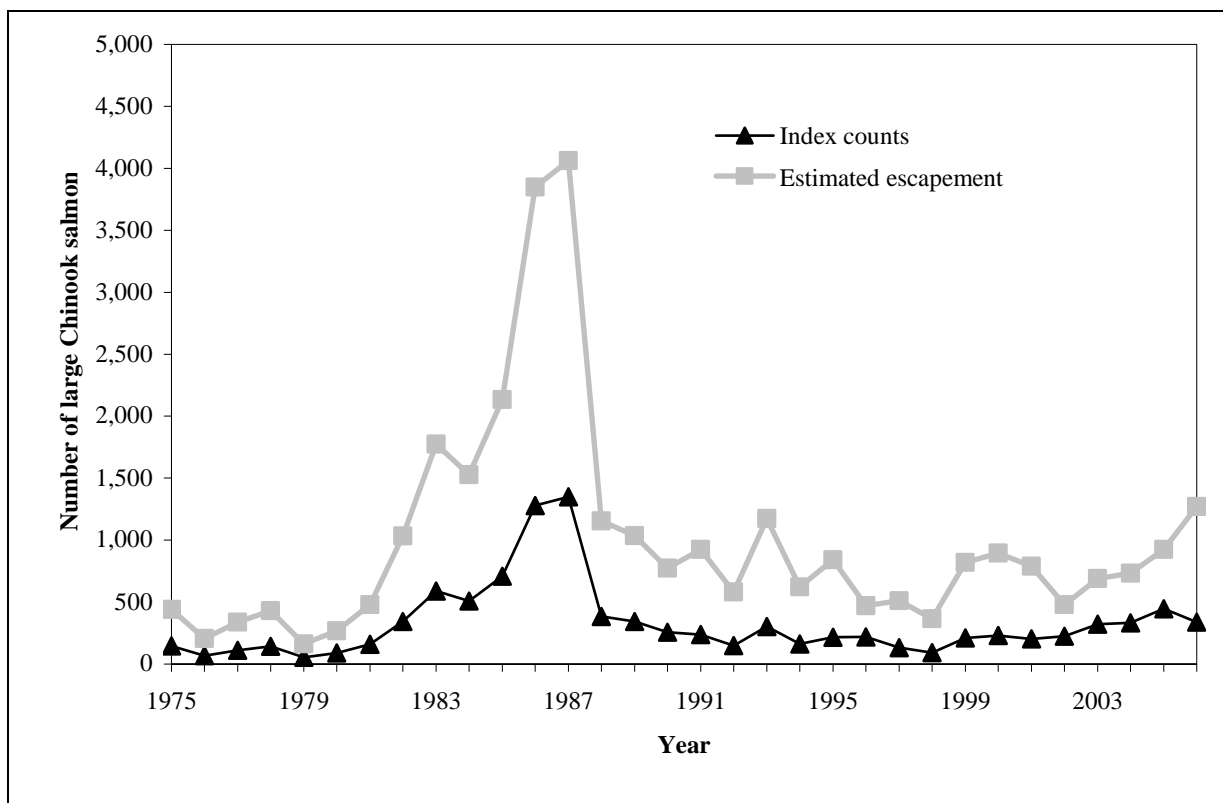


Figure 6.—Index counts and preferred estimates of spawning abundance for large (≥ 660 mm MEF) Chinook salmon in the Blossom River, 1975–2006.

inability to capture adequate numbers of smaller fish during Event 2. Fish are captured during Event 2 by “blind” casting into relatively deep water with known concentrations of fish, which are generally not visible to the fisher. These conditions favor snagging larger fish as a simple function of size. Also, fish <660 mm MEF are generally jacks, which tend to be opportunistic spawners, and as such tend to “spook” easily as they avoid aggressive displays by larger males attending females on redds. As a result of this behavior, jacks may be less susceptible to snagging than females guarding redds or larger males attending females. Because the pre-spawn and spawning areas are in relatively fast deep water, no alternative method has been devised to capture these fish more effectively than that currently used. Fish are captured during Event 1 using bait casting techniques, which are ineffective during Event 2 when fish are spawning, or nearly so. Fish captured during Event 1 are likely to be a more representative

sample of the relative abundance of medium sized fish than those captured during Event 2, as the use of bait should not be particularly conducive to size-selective sampling.

CONCLUSIONS AND RECOMMENDATIONS

This marks the fourth and final year of Chinook salmon M–R experiments on the Blossom River. These studies were designed to estimate the abundance and age, sex, length composition of large spawners, and to calculate an expansion factor that could be used to expand peak aerial survey counts of large spawners to estimates of spawning abundance. We recommend that the resulting mean expansion factor (3.01, SE = 1.03) be used to estimate the abundance of large spawners in years when no survey condition information is available. We further recommend that the average (3.87, SE = 0.62) of the two annual expansion factors estimated in years when

surveys were conducted under normal conditions (1998 and 2006) be used to estimate spawning abundance in years when conditions are normal. In years when the survey conditions were rated excellent, the average of the 2004 and 2005 annual expansion factors (2.14, SE = 0.19) should be used to estimate spawning abundance.

Although we would prefer to have at least one additional year of estimates under both normal and excellent survey conditions in accordance with USCTC standards, we believe this to be the most accurate method of estimating spawning abundance at present. We recommend that annual survey counts and escapement ASL sampling be continued.

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APPENDIX A

Appendix A1.—Detection of size- and/or sex-selective sampling during a two-sample mark–recapture experiment and its effects on estimation of population size and population composition.

Size selective sampling: The Kolmogorov-Smirnov two sample test (Conover 1980) is used to detect significant evidence that size selective sampling occurred during the first and/or second sampling events. The second sampling event is evaluated by comparing the length frequency distribution of all fish marked during the first event (M) with that of marked fish recaptured during the second event (R) by using the null test hypothesis of no difference. The first sampling event is evaluated by comparing the length frequency distribution of all fish inspected for marks during the second event (C) with that of R. A third test that compares M and C is then conducted and used to evaluate the results of the first two tests when sample sizes are small. Guidelines for small sample sizes are <30 for R and <100 for M or C.

Sex selective sampling: Contingency table analysis (χ^2 -test) is generally used to detect significant evidence that sex selective sampling occurred during the first and/or second sampling events. The counts of observed males to females are compared between M&R, C&R, and M&C using the null hypothesis that the probability that a sampled fish is male or female is independent of sample. If the proportions by gender are estimated for a sample (usually C), rather than observed for all fish in the sample, contingency table analysis is not appropriate and the proportions of females (or males) are then compared between samples using a two sample test (e.g. Student's t-test).

M vs. R	C vs. R	M vs. C
<i>Case I:</i>		
Fail to reject H_0	Fail to reject H_0	Fail to reject H_0
There is no size/sex selectivity detected during either sampling event.		

<i>Case II:</i>		
Reject H_0	Fail to reject H_0	Reject H_0
There is no size/sex selectivity detected during the first event but there is during the second event sampling.		

<i>Case III:</i>		
Fail to reject H_0	Reject H_0	Reject H_0
There is no size/sex selectivity detected during the second event but there is during the first event sampling.		

<i>Case IV:</i>		
Reject H_0	Reject H_0	Either result possible
There is size/sex selectivity detected during both the first and second sampling events.		

<i>Evaluation Required:</i>		
Fail to reject H_0	Fail to reject H_0	Reject H_0

Sample sizes and powers of tests must be considered:

-continued-

- A. If sample sizes for M vs. R and C vs. R tests are not small and sample sizes for M vs. C test are very large, the M vs. C test is likely detecting small differences which have little potential to result in bias during estimation. Case I is appropriate.
- B. If a) sample sizes for M vs. R are small, b) the M vs. R p-value is not large (~ 0.20 or less), and c) the C vs. R sample sizes are not small and/or the C vs. R p-value is fairly large (~ 0.30 or more), the rejection of the null in the M vs. C test was likely the result of size/sex selectivity during the second event which the M vs. R test was not powerful enough to detect. *Case I* may be considered but *Case II* is the recommended, conservative interpretation.
- C. If a) sample sizes for C vs. R are small, b) the C vs. R p-value is not large (~ 0.20 or less), and c) the M vs. R sample sizes are not small and/or the M vs. R p-value is fairly large (~ 0.30 or more), the rejection of the null in the M vs. C test was likely the result of size/sex selectivity during the first event which the C vs. R test was not powerful enough to detect. *Case I* may be considered but *Case III* is the recommended, conservative interpretation. D. If a) sample sizes for C vs. R and M vs. R are both small, and b) both the C vs. R and M vs. R p-values are not large (~ 0.20 or less), the rejection of the null in the M vs. C test may be the result of size/sex selectivity during both events which the C vs. R and M vs. R tests were not powerful enough to detect. *Cases I, II, or III* may be considered but *Case IV* is the recommended, conservative interpretation.

Case I. Abundance is calculated using a Petersen-type model from the entire data set without stratification. Composition parameters may be estimated after pooling length, sex, and age data from both sampling events.

Case II. Abundance is calculated using a Petersen-type model from the entire data set without stratification. Composition parameters may be estimated using length, sex, and age data from the first sampling event without stratification. If composition is estimated from second event data or after pooling both sampling events, data must first be stratified to eliminate variability in capture probability (detected by the M vs. R test) within strata. Composition parameters are estimated within strata, and abundance for each stratum needs to be estimated using a Petersen-type formula. Overall composition parameters are estimated by combining stratum estimates weighted by estimated stratum abundance according to the formulae below.

Case III. Abundance is calculated using a Petersen-type model from the entire data set without stratification. Composition parameters may be estimated using length, sex, and age data from the second sampling event without stratification. If composition is estimated from first event data or after pooling both sampling events, data must first be stratified to eliminate variability in capture probability (detected by the C vs. R test) within strata. Composition parameters are estimated within strata, and abundance for each stratum needs to be estimated using a Petersen-type formula. Overall composition parameters are estimated by combining stratum estimates weighted by estimated stratum abundance according to the formulae below.

Case IV. Data must be stratified to eliminate variability in capture probability within strata for at least one or both sampling events. Abundance is calculated using a Petersen-type model for each stratum, and estimates are summed across strata to estimate overall abundance. Composition parameters may be estimated within the strata as determined above, but only using data from sampling events where stratification has eliminated variability in capture probabilities within strata. If data from both sampling events are to be used, further stratification may be necessary to meet the condition of capture homogeneity within strata for both events. Overall composition parameters are estimated by combining stratum estimates weighted by estimated stratum abundance.

If stratification by sex or length is necessary prior to estimating composition parameters, then an overall composition parameters (p_w) is estimated by combining within stratum composition estimates using:

-continued-

$$\hat{p}_w = \sum_{z=1}^j \frac{\hat{N}_z}{\hat{N}_\Sigma} \hat{p}_{zw} \quad (1)$$

$$\hat{V}[\hat{p}_w] \approx \frac{1}{\hat{N}_\Sigma^2} \left(\sum_{z=1}^j \hat{N}_z^2 \hat{V}[\hat{p}_{zw}] + (\hat{p}_{zw} - \hat{p}_w)^2 \hat{V}[\hat{N}_z] \right). \quad (2)$$

where:

- j = the number of sex/size strata;
- \hat{p}_{zw} = the estimated proportion of fish that were age or size w among fish in stratum z ;
- \hat{N}_i = the estimated abundance in stratum i ; and,
- \hat{N}_Σ = sum of the \hat{N}_i across strata.

Appendix A2.—Tests of consistency for the Petersen estimator (from Seber 1982, page 438).

Of the following conditions, at least one must be fulfilled to meet assumptions of a Petersen estimator:

1. Marked fish mix completely with unmarked fish between events;
2. Every fish has an equal probability of being captured and marked during event 1; or,
3. Every fish has an equal probability of being captured and examined during event 2.

To evaluate these three assumptions, the chi-square statistic will be used to examine the following contingency tables as recommended by Seber (1982). At least one null hypothesis needs to be accepted for assumptions of the Petersen model (Bailey 1951, 1952; Chapman 1951) to be valid. If all three tests are rejected, a temporally or geographically stratified estimator (Darroch 1961) should be used to estimate abundance.

I.-Test for complete mixing ^a

Area/time where marked	Time/area where recaptured				Not recaptured (n ₁ -m ₂)
	1	2	...	t	
1					
2					
...					
s					

II.-Test for equal probability of capture during the first event ^b

	Area/time where examined			
	1	2	...	t
Marked (m ₂)				
Unmarked (n ₂ -m ₂)				

III.-Test for equal probability of capture during the second event ^c

	Area/time where marked			
	1	2	...	s
Recaptured (m ₂)				
Not recaptured (n ₁ -m ₂)				

^a This tests the hypothesis that movement probabilities (θ) from time or area i ($i = 1, 2, \dots, s$) to section j ($j = 1, 2, t$) are the same among sections: $H_0: \theta_{ij} = \theta_j$.

^b This tests the hypothesis of homogeneity on the columns of the 2-by-t contingency table with respect to the marked to unmarked ratio among time or area designations: $H_0: \sum_i a_i \theta_{ij} = k U_j$, where k = total marks released/total unmarked in the population, U_j = total unmarked fish in stratum j at the time of sampling, and a_i = number of marked fish released in stratum i .

^c This tests the hypothesis of homogeneity on the columns of this 2-by-s contingency table with respect to recapture probabilities among time or area designations: $H_0: \sum_j \theta_{ij} p_j = d$, where p_j is the probability of capturing a fish in section j during the second event, and d is a constant.

Appendix A3.—Predicting escapement from index counts using an expansion factor.

The expansion factor provides a means of predicting escapement in years where only an index count of the escapement is available, i.e. no weir counts or mark–recapture experiments were conducted. The expansion factor is the average over several years of the ratio of the escapement estimate (or weir count) to the index count.

Systems where escapement is known

On systems where escapement can be completely enumerated with weirs or other complete counting methods, the expansion factor is an estimate of the expected value of the “population” of annual expansion factors (π ’s) for that system:

$$\bar{\pi} = \frac{\sum_{y=1}^k \pi_y}{k} \quad (1)$$

where $\pi_y = N_y / C_y$ is the observed expansion factor in year y , N_y is the known escapement in year y , C_y is the index count in year y , and k is the number of years for which these data are available to calculate an annual expansion factor.

The estimated variance for expansion of index counts needs to reflect two sources of uncertainty for any predicted value of π , (π_p). First is an estimate of the process error ($var(\pi)$); the variation across years in the π ’s, reflecting, for example, weather or observer-induced effects on how many fish are counted in a survey for a given escapement. Second is the sampling variance of $\bar{\pi}$ ($var(\bar{\pi})$), which will decline as we collect more data pairs.

The variance for prediction will be estimated (Neter et al. 1990):

$$\hat{var}(\pi_p) = \hat{var}(\pi) + \hat{var}(\bar{\pi}) \quad (2)$$

where:

$$\hat{var}(\pi) = \frac{\sum_{y=1}^k (\pi_y - \bar{\pi})^2}{k - 1} \quad (3)$$

and:

$$\hat{var}(\bar{\pi}) = \frac{\sum_{y=1}^k (\pi_y - \bar{\pi})^2}{k(k - 1)} \quad (4)$$

such that:

$$\hat{var}(\pi_p) = \frac{\sum_{y=1}^k (\pi_y - \bar{\pi})^2}{k - 1} + \frac{\sum_{y=1}^k (\pi_y - \bar{\pi})^2}{k(k - 1)} \quad (5)$$

-continued-

Systems where escapement is estimated

On systems where escapement is estimated, the expansion factor is an estimate of the expected value of the “population” of annual expansion factors (π ’s) for that system:

$$\bar{\pi} = \frac{\sum_{y=1}^k \hat{\pi}_y}{k} \quad (6)$$

where $\hat{\pi}_y = \hat{N}_y / C_y$ is the estimate of the expansion factor in year y , \hat{N}_y is the estimated escapement in year y , and other terms are as described above.

The variance for prediction will again be estimated:

$$\hat{var}(\pi_p) = \hat{var}(\pi) + \hat{var}(\bar{\pi}) \quad (7)$$

The estimate of $var(\pi)$ should again reflect only process error. Variation in $\hat{\pi}$ across years, however, represents process error **plus** measurement error within years (e.g. the mark-recapture induced error in escapement estimation) and is described by the relationship (Mood et al. 1974):

$$V(\hat{\pi}) = V[E(\hat{\pi})] + E[V(\hat{\pi})] \quad (8)$$

This relationship can be rearranged to isolate process error, that is:

$$V[E(\hat{\pi})] = V[\hat{\pi}] - E[V(\hat{\pi})] \quad (9)$$

An estimate of $var(\pi)$ representing only process error therefore is:

$$\hat{var}(\pi) = \hat{var}(\hat{\pi}) - \frac{\sum_{y=1}^k \hat{var}(\hat{\pi}_y)}{k} \quad (10)$$

where $\hat{var}(\hat{\pi}_y) = \hat{var}(\hat{N}_y) / C_y^2$ and $\hat{var}(\hat{N}_y)$ is obtained during the experiment when N_y is estimated. We can calculate:

$$\hat{var}(\hat{\pi}) = \frac{\sum_{y=1}^k (\hat{\pi}_y - \bar{\pi})^2}{k - 1} \quad (11)$$

-continued-

and we can estimate $var(\bar{\pi})$ similarly to as we did above:

$$\hat{var}(\bar{\pi}) = \frac{\sum_{y=1}^k (\hat{\pi}_y - \bar{\pi})^2}{k(k-1)} \quad (12)$$

where both process and measurement errors need to be included.

For large k ($k > 30$), equations (11) and (12) provide reasonable parameter estimates, however for small k the estimates are imprecise and may result in negative estimates of variance when the results are applied as in equation (7).

Because k is typically < 10 , we will estimate $var(\hat{\pi})$ and $var(\bar{\pi})$ using parametric bootstrap techniques Efron and Tibshirani 1993. The sampling distributions for each of the $\hat{\pi}_y$ are modeled using Normal distributions with means $\hat{\pi}_y$ and variances $\hat{var}(\hat{\pi}_y)$. At each bootstrap iteration, a bootstrap value $\hat{\pi}_{y(b)}$ is drawn from each of these Normal distributions and the bootstrap value $\hat{\pi}_{(b)}$ is randomly chosen from the k values of $\hat{\pi}_{y(b)}$. Then, a bootstrap sample of size k is drawn from the k values of $\hat{\pi}_{y(b)}$ by sampling with replacement, and the mean of this bootstrap is the bootstrap value $\bar{\pi}_{(b)}$. This procedure is repeated $B = 1,000,000$ times. We can then estimate $var(\hat{\pi})$ using:

$$\hat{var}_B(\hat{\pi}) = \frac{\sum_{b=1}^B (\hat{\pi}_{(b)} - \overline{\hat{\pi}_{(b)}})^2}{B-1} \quad (13)$$

where:

$$\overline{\hat{\pi}_{(b)}} = \frac{\sum_{b=1}^B \hat{\pi}_{(b)}}{B} \quad (14)$$

and we can calculate $var_B(\bar{\pi})$ using equations (13) and (14) with appropriate substitutions. The variance for prediction is then estimated:

$$\hat{var}(\pi_p) = \hat{var}_B(\hat{\pi}) - \frac{\sum_{y=1}^k \hat{var}(\hat{\pi}_y)}{k} + \hat{var}_B(\bar{\pi}) \quad (15)$$

As the true sampling distributions for the $\hat{\pi}_y$ are typically skewed right, using a Normal distribution to approximate these distributions in the bootstrap process will result in estimates of $var(\hat{\pi})$ and $var(\bar{\pi})$ that are biased slightly high, but simulation studies using values similar to those realized for this application indicated that the bias in equation (15) is $< 1\%$.

Predicting Escapement

In years when an index count (C_p) is available but escapement (N_p) is not known, it can be predicted:

$$\hat{N}_p = \bar{\pi} C_p \quad (16)$$

and:

$$\text{var}(\hat{N}_p) = C_p^2 \text{var}(\pi_p) \quad (17)$$

Appendix A4.—Age by sex of small (<500 mm MEF), medium (500–659 mm MEF), and large (≥660 mm MEF) Chinook salmon sampled during Event 1 (PANEL A) and Event 2 (PANEL B) in the Blossom River, 2006. Includes all samples from which age and length was determined.

PANEL A: EVENT 1													
			Brood year and age class										
			2004	2003	2003	2003	2002	2002	2001	2001	2000	1999	
			0.1	0.2	1.1	2.0	0.3	1.2	0.4	1.3	1.4	1.5	Total
Small	Male	Sample size	3		44								47
		Percent	6.4		93.6								100.0
	Total	Sample size	3		44								47
		Percent	6.4		93.6								100.0
Medium	Male	Sample size	1	3	4	20							28
		Percent	3.6	10.7	14.3	71.4							100.0
	Total	Sample size	1	3	4	20							28
		Percent	3.6	10.7	14.3	71.4							100.0
Large	Male	Sample size		1			5	34		35	4	1	80
		Percent		0.6			3.0	20.7		21.3	2.4	0.6	48.8
	Female	Sample size					7	1	1	61	14		84
		Percent					4.3	0.6	0.6	37.2	8.5		51.2
	Total	Sample size		1			12	35	1	96	18	1	164
		Percent		0.6			7.3	21.3	0.6	58.5	11.0	0.6	100.0
Total	Male	Sample size	4	4	48	20	5	34		35	4	1	155
		Percent	1.7	1.7	20.1	8.4	2.1	14.2		14.6	1.7	0.4	64.9
	Female	Sample size					7	1	1	61	14		84
		Percent					2.9	0.4	0.4	25.5	5.9		35.1
	Total	Sample size	4	4	48	20	12	35	1	96	18	1	239
		Percent	1.7	1.7	20.1	8.4	5.0	14.6	0.4	40.2	7.5	0.4	100.0
PANEL B: EVENT 2													
			Brood year and age class										
			2004	2003	2003	2003	2002	2002	2001	2001	2000	1999	
			0.1	0.2	1.1	2.0	0.3	1.2	0.4	1.3	1.4	1.5	Total
Small	Male	Sample size				1				1			2
		Percent				50.0				50.0			100.0
	Total	Sample size				1				1			2
		Percent				50.0				50.0			100.0
Medium	Male	Sample size		1				1					2
		Percent		50.0				50.0					100.0
	Total	Sample size		1				1					2
		Percent		50.0				50.0					100.0
Large	Male	Sample size					6	25		49	8	1	89
		Percent					3.5	14.7		28.8	4.7	0.6	52.4
	Female	Sample size					3		1	54	22	1	81
		Percent					1.8		0.6	31.8	12.9	0.6	47.6
	Total	Sample size					9	25	1	103	30	2	170
		Percent					5.3	14.7	0.6	60.6	17.6	1.2	100.0
Total	Male	Sample size		1		1	6	26		50	8	1	93
		Percent		0.6		0.6	3.4	14.9		28.7	4.6	0.6	53.4
	Female	Sample size					3		1	54	22	1	81
		Percent					1.7		0.6	31.0	12.6	0.6	46.6
	Total	Sample size		1		1	9	26	1	104	30	2	174
		Percent		0.6		0.6	5.2	14.9	0.6	59.8	17.2	1.1	100.0

Appendix A5.—Computer files used to estimate the spawning abundance and age, sex, length composition of Chinook salmon in the Blossom River in 2006.

File name	Description
06Blos41A.xls	Spreadsheets containing Tables 1–5, Figure 5, Appendix A4, and chi-square data.
06Blos41B.xls	Spreadsheet containing Table 6, Figure 2, and Figure 5.
Blos06MR41asl.xls	Spreadsheets containing mark–recapture data file.
KSN1M2.xls	Spreadsheets containing Kolmogorov-Smirnov 2-sample test results for marked versus recaptured fish.
KSN2M2.xls	Spreadsheets containing Kolmogorov-Smirnov 2-sample test results for inspected versus recaptured fish.